中国，天山ウルムチ No.1 氷河における微生物相と硝化・脱窒遺伝子解析

瀬川高弘（極地研、融合）[1,2]、石井聡（北大）[3]、本山秀明（極地研）[1]、
本郷裕一（東工大）[4]、竹内望（千葉大）[5]
[1] *国立極地研究所*, [2] *新領域融合研究センター*, [3] *北海道大学　工学研究院*
[4] *東京工業大学　生命理工学研究科*, [5] *千葉大学　理学研究科*

Impact of microbial communities on nitrogen cycles on Urumqi Glacier No.1 in China

Takahiro Segawa[1,2], Satoshi Ishii[3], Hideaki Motoyama[1], Yuichi Hongoh[4], and Nozomu Takeuchi[5]
[1]*National Institute of Polar Research*
[2]*Transdisciplinary research integration center*
[3]*Facultuy of Engineering, Hokkaido University*
[4]*Graduate School of Bioscience and Biotechnology, Tokyo Institute of Technology*
[5]*Graduate School of Science, Chiba University*

Many kinds of microorganisms, including snow algae and bacteria, have been found on glaciers in various parts of the world. However, our knowledge of the nitrogen cycling microbial communities of the glacier ecosystems is still very limited. In order to clarify distributions of ammonia-oxidizing and denitrifying microorganisms on Urumqi. Glacier No.1 in China, we analyzed DNA and RNA using molecular genetic tools, including pyrosequencing of 16S rRNA gene PCR amplicons.

Analysis of 16S rRNA genes revealed the presence of ~400 bacterial OTUs on the glacial surface. Based on the dominant phylotypes and UniFrac analysis, the bacterial community on the glacier could be divided into three types, corresponding to the snow-covered, snow- and ice-covered, and bare-ice areas of the glacier. The glacial samples contained nitrifying bacteria such as genera Nitrosomonas, Nitrosospira, Candidatus Nitrotoga and a large number of unclassified genera in Nitrosomonadaceae. Quantitative digital PCR of nitrifying and nitrate reducing genes revealed that copy numbers of ammonia oxidizers and nitrate reducers showed altitudinal distribution on the glacier. This study yields an initial insight into the glacial ecosystem of bacteria carrying genes for the nitrifying and denitrification pathway in a glacial environment.